



Nucleotide

Protein

formatting **BLAST**

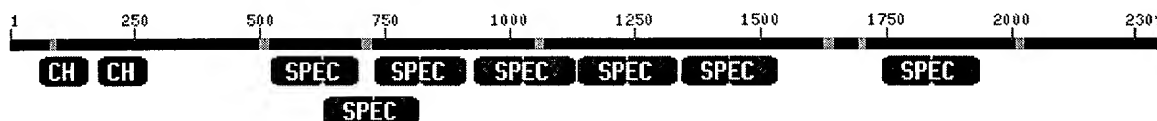
Translations

Retrieve results for an
RID

WARNING: 6 illegal characters were removed: 6 Os

Your request has been successfully submitted and put into the Blast Queue.

Query = (2309 letters)

Putative conserved domains have been detected, click on the image below for detailed results.

The request ID is 1085768146-22635-169323450554.BLASTQ3

Format! or **Reset all**

The results are estimated to be ready in 23 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

FormatShow ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment in HTMLUse new formatter ☐ Masking Character Default(X for protein, n for nucleotide) Masking Color Black

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Format for PSI-BLAST ☐ with inclusion threshold: 0.005Limit results by or select from: All organisms



results of BLAST

BLASTP 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1085768146-22635-169323450554.BLASTQ3

Query=

(2309 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples

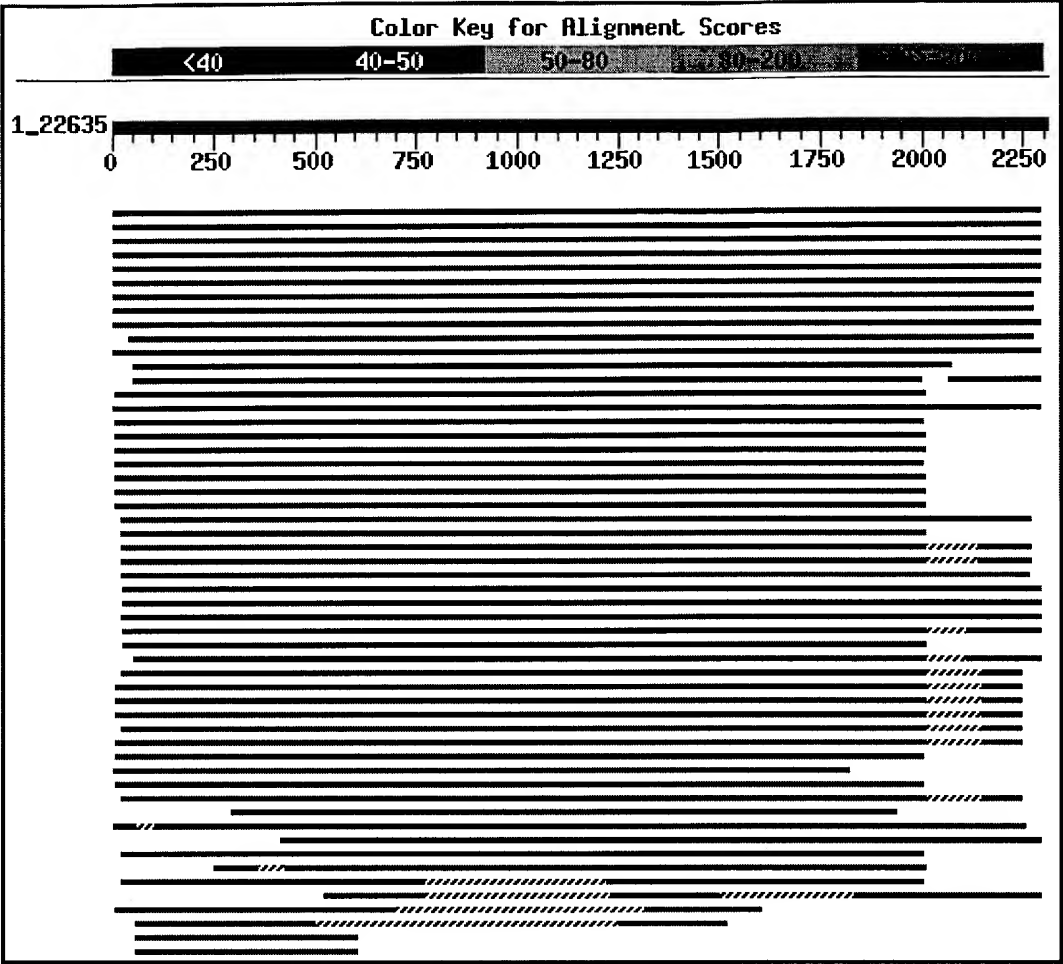
1,843,811 sequences; 610,536,048 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)






















Distribution of 253 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:			Score (bits)	E Value	
<u>gi 47227240 emb CAG00602.1 </u>	unnamed protein product [Tetrao...	<u>2284</u>	0.0		
<u>gi 38084794 ref XP_129130.3 </u>	spectrin beta 3 [Mus musculus]	<u>3411</u>	0.0	L	
<u>gi 31201699 ref XP_309797.1 </u>	ENSANGP00000023406 [Anopheles ...	<u>1576</u>	0.0		
<u>gi 47209542 emb CAF96656.1 </u>	unnamed protein product [Tetrao...	<u>1895</u>	0.0		
<u>gi 39594389 emb CAE71967.1 </u>	Hypothetical protein CBG19038 [...	<u>1446</u>	0.0		
<u>gi 25154697 ref NP_504749.2 </u>	beta-G spectrin, UNCoordinated...	<u>1407</u>	0.0	L	
<u>gi 7505762 pir T29140</u>	hypothetical protein K11C4.3 - Caeno...	<u>1395</u>	0.0		
<u>gi 423777 pir A46147</u>	spectrin beta chain - fruit fly (Dros...	<u>1521</u>	0.0	L	
<u>gi 47221201 emb CAG13137.1 </u>	unnamed protein product [Tetrao...	<u>1660</u>	0.0		
<u>gi 33340563 gb AAQ14859.1 </u>	beta spectrin IV [Homo sapiens]	<u>1207</u>	0.0	L	
<u>gi 17647191 ref NP_523388.1 </u>	CG5870-PA [Drosophila melanoga...	<u>1519</u>	0.0	L	
<u>gi 11066461 gb AAG28596.1 </u>	spectrin-like protein GTRAP41 [R...	<u>3498</u>	0.0	L	
<u>gi 29179635 gb AAH48851.1 </u>	Similar to beta-spectrin 3 [Mus ...	<u>1112</u>	0.0		
<u>gi 134798 sp P11277 SPCB_HUMAN</u>	Spectrin beta chain, erythro...	<u>1660</u>	0.0	L	
<u>gi 30348966 ref NP_787030.1 </u>	spectrin beta 2 isoform 1; bet...	<u>2134</u>	0.0	L	
<u>gi 17368942 sp Q9H254 SPCQ_HUMAN</u>	Spectrin beta chain, brain...	<u>1316</u>	0.0	L	
<u>gi 30315658 ref NP_842565.1 </u>	spectrin, beta, non-erythrocyt...	<u>2009</u>	0.0	L	
<u>gi 18859423 ref NP_571600.1 </u>	spectrin, beta, erythrocytic; ...	<u>1818</u>	0.0	L	

gi 30794220 ref NP_115999.1 	spectrin beta 4; beta-spectrin...	1317	0.0	L
gi 40353204 ref NP_066022.1 	spectrin, beta, non-erythrocyt...	1308	0.0	L
gi 13435161 ref NP_079489.1 	spectrin, beta, non-erythrocyt...	1313	0.0	L
gi 47210379 emb CAF95574.1 	unnamed protein product [Tetrao...	1133	0.0	
gi 33303722 gb AAQ02380.1 	non-erythroid spectrin beta [Rat...	2152	0.0	
gi 476928 pir A47213	beta-fodrin - human (fragment) >gi 42...	1177	0.0	L
gi 17367415 sp Q9QWN8 SPCP RAT	Spectrin beta chain, brain 2...	3472	0.0	L
gi 11992162 gb AAG42473.1 	spectrin beta IV [Homo sapiens]	1316	0.0	L
gi 5734146 gb AAD49858.1 	beta-G spectrin [Caenorhabditis e...	1455	0.0	L
gi 47058982 ref NP_997687.1 	erythroid spectrin beta [Rattu...	1645	0.0	L
gi 2506246 sp P15508 SPCB MOUSE	Spectrin beta chain, erythr...	1634	0.0	L
gi 34855389 ref XP_218364.2 	similar to betaIV-spectrin sig...	1197	0.0	L
gi 17562506 ref NP_504748.1 	beta-G spectrin, UNCoordinated...	1409	0.0	L
gi 11602890 gb AAF93173.1 	betaIV spectrin isoform sigma4 [...	1302	0.0	L
gi 16117405 gb AAK38731.1 	beta4-spectrin [Mus musculus] >g...	1313	0.0	L
gi 448251 prf 1916380A	beta spectrin (beta fodrin)	2085	0.0	
gi 7106421 ref NP_033286.1 	spectrin beta 2 isoform 2; beta...	2008	0.0	L
gi 34866100 ref XP_234322.2 	similar to Spectrin beta chain...	1653	0.0	L
gi 17976528 gb AAK77612.2 	Uncoordinated protein 70, isofo...	1454	0.0	
gi 28277312 gb AAH46267.1 	LOC398511 protein [Xenopus laevis]	1223	0.0	L
gi 34879632 ref XP_240072.2 	similar to Spectrin beta chain...	2131	0.0	L
gi 9507135 ref NP_062040.1 	beta-spectrin 3 [Rattus norvegi...	3471	0.0	L
gi 5902122 ref NP_008877.1 	spectrin, beta, non-erythrocyti...	3308	0.0	L
gi 27413156 ref NP_000338.2 	spectrin, beta, erythrocytic (...	1664	0.0	L
gi 4507195 ref NP_003119.1 	spectrin, beta, non-erythrocyti...	2182	0.0	L
gi 338440 gb AAA60578.1 	spectrin Rouen (beta-220-218) muta...	1667	0.0	L
gi 15213122 gb AAK85734.1 	beta-G spectrin [Brugia malayi]	1490	0.0	
gi 31201697 ref XP_309796.1 	ENSANGP00000012507 [Anopheles ...	1523	0.0	
gi 40216167 gb AAR82828.1 	AT24411p [Drosophila melanogaster]	1071	0.0	
gi 47221024 emb CAG12718.1 	unnamed protein product [Tetrao...	911	0.0	
gi 11602887 gb AAF93171.1 	betaIV spectrin isoform sigma2 [...	859	0.0	L
gi 10047361 dbj BAB13468.1 	KIAA1642 protein [Homo sapiens]	843	0.0	L
gi 226515 prf 1516310A	beta spectrin	766	0.0	
gi 338330 gb AAA63259.1 	muscle beta spectrin	748	0.0	
gi 2511779 gb AAC79502.1 	beta III spectrin [Homo sapiens]	665	0.0	L
gi 31209523 ref XP_313728.1 	ENSANGP00000017034 [Anopheles ...	524	e-146	
gi 45552921 ref NP_995987.1 	CG12008-PC [Drosophila melanog...	506	e-141	
gi 45552923 ref NP_995988.1 	CG12008-PB [Drosophila melanog...	506	e-141	
gi 18481635 gb AAL73492.1 	beta I spectrin form betaI sigma...	505	e-141	
gi 24656802 ref NP_523900.1 	CG12008-PA [Drosophila melanog...	505	e-141	L
gi 7706190 ref NP_057726.1 	spectrin, beta, non-erythrocyti...	500	e-139	L
gi 7655 emb CAA37939.1 	betaH spectrin [Drosophila melanoga...	496	e-138	L
gi 420115 pir S29854	spectrin beta chain - dog (fragment) ...	496	e-138	L
gi 103502 pir A37792	spectrin beta-H chain - fruit fly (Dr...	488	e-136	
gi 444793 prf 1908227A	beta spectrin	488	e-135	
gi 11602888 gb AAF93172.1 	betaIV spectrin isoform sigma3 [...	481	e-134	L
gi 7506776 pir T23630	hypothetical protein R31.1 - Caenorh...	464	e-128	
gi 25155104 ref NP_741632.1 	SMAll body size SMA-1, betaH c...	462	e-128	L
gi 39592126 emb CAE75346.1 	Hypothetical protein CBG23326 [...	455	e-126	

gi 18147604 dbj BAB83244.1 	betaIV-spectrin sigma6-A [Mus m...	447	e-123	
gi 34856723 ref XP_238278.2 	similar to Spectrin beta chain...	412	e-113	
gi 2511781 gb AAC79503.1 	beta III spectrin [Homo sapiens]	348	1e-93	
gi 11992164 gb AAG42474.1 	spectrin beta IV [Homo sapiens]	337	2e-90	
gi 41054603 ref NP_955880.1 	actinin alpha 4; wu:fb53f05 [D...	336	5e-90	
gi 24639240 ref NP_726784.1 	CG4376-PB [Drosophila melanoga...	333	4e-89	
gi 24639238 ref NP_477484.2 	CG4376-PA [Drosophila melanoga...	332	6e-89	
gi 8186 emb CAA36042.1 	unnamed protein product [Drosophila...	332	9e-89	
gi 13123941 sp Q9QXQ0 AAC4_RAT	Alpha-actinin 4 (Non-muscle ...	331	1e-88	
gi 11230802 ref NP_068695.1 	actinin alpha 4 [Mus musculus]...	331	1e-88	
gi 45384104 ref NP_990457.1 	alpha-actinin [Gallus gallus] ...	330	2e-88	
gi 1070611 pir FAFFAA	alpha-actinin - fruit fly (Drosophil...	330	2e-88	
gi 45387533 ref NP_991107.1 	Unknown (protein for MGC:77243...	330	2e-88	
gi 47212235 emb CAF96202.1 	unnamed protein product [Tetrao...	330	3e-88	
gi 25992501 gb AAN77132.1 	alpha-actinin [Danio rerio] >gi ...	330	3e-88	
gi 38197444 gb AAH61788.1 	Actn4 protein [Rattus norvegicus]	329	4e-88	
gi 12025678 ref NP_004915.2 	actinin, alpha 4 [Homo sapiens...	329	4e-88	
gi 2804273 dbj BAA24447.1 	alpha actinin 4 [Homo sapiens]	328	7e-88	
gi 31242387 ref XP_321624.1 	ENSANGP00000011796 [Anopheles...	328	8e-88	
gi 32766313 gb AAH54911.1 	Zgc:63559 protein [Danio rerio]	326	5e-87	
gi 37362178 gb AAQ91217.1 	actinin, alpha 2 [Danio rerio]	325	1e-86	
gi 17137758 ref NP_477485.1 	CG4376-PC [Drosophila melanoga...	324	1e-86	
gi 625303 pir FAHUAA	alpha-actinin 1 - human >gi 28334 emb...	324	1e-86	
gi 4501891 ref NP_001093.1 	actinin, alpha 1 [Homo sapiens]...	324	2e-86	
gi 30585329 gb AAP36937.1 	Homo sapiens actinin, alpha 1 [s...	324	2e-86	
gi 38018016 gb AAR08137.1 	brain-specific alpha actinin 1 i...	323	3e-86	
gi 13928936 ref NP_113863.1 	alpha actinin 4; alpha actinin...	323	4e-86	
gi 13591902 ref NP_112267.1 	actinin, alpha 1; non-muscle a...	322	5e-86	
gi 2345081 gb AAC02791.1 	beta-spectrin [Homo sapiens]	322	6e-86	
gi 539494 pir A42162	alpha-actinin 1 - chicken >gi 211083 ...	322	7e-86	
gi 13124665 sp P05094 AAC1_CHICK	Alpha-actinin 1 (Alpha-act...	322	7e-86	
gi 46395721 sp Q7TPR4 AAC1_MOUSE	Alpha-actinin 1 (Alpha-act...	322	9e-86	
gi 4557241 ref NP_001095.1 	skeletal muscle specific actini...	321	1e-85	

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|47227240|emb|CAG00602.1|](#) unnamed protein product [Tetraodon nigroviridis]
Length = 2413

Score = 2284 bits (5918), Expect = 0.0

Identities = 1439/2429 (59%), Positives = 1695/2429 (69%), Gaps = 170/2429 (6%)

Query: 3 STLSPDTDFDSLEIQGQYSDINNRWDL P-DSDWDNDSSSARLFERSRI----- 48

ST+SPTDFDSLEIQ QY+DINNRWDL ++DWDN++SSARLFERSRI

Sbjct: 1 STISPTDFDSLEIQQQYNDINNRWDLAAETDWDNENSSARLFERSRIKALAAMDWDHRNR 60

Query: 49 -----MLADEREAVQKKTFTKWVNSHLARVTCRVGDLYSXX 84

```

                                L DEREAVQKKTFFTKWVNSHL RVTCT+GDLY+
Sbjct: 61  EPSPSPAAAFVNQVQYANILEGRFKQLQDEREAVQKKTFFTKWVNSHLGRVTCRIGDLYTDL 120

Query: 85  XXXXXXXXXXXXEVLSGETLPKPTKGRMRIHCLENVD--LQFLKEQKVHLENMGSHDIVDGN 142
          EVLSGE LP+PTKGRMRIHCLENVD LQFLKEQKVHLENMGSHDIVDGN
Sbjct: 121  RDGRMLIRLLEVLSGEQLPRPTKGRMRIHCLENVDKALQFLKEQKVHLENMGSHDIVDGN 180

Query: 143  HRLTLGLVWTIILRFQIQDISVETEDNKEKKSADALLWCQMKTAGYPNVNVHNFSTSW 202
          HRLTLGL+WTIILRFQIQDISVETEDNKEKKSADALLWCQMKTAGYPNVN+HNFSTSW
Sbjct: 181  HRLTLGLIWTIILRFQIQDISVETEDNKEKKSADALLWCQMKTAGYPNVNIHNFSTSW 240

Query: 203  RDGLAFNAIVHKHRPDLDFESLKKCAHYNLQNAFNAEKEGLTKLLDPEDVNVDQPD 262
          RDGLAFNAIVHKHRPDL+DFE+LK+ NAHYNLQNAFN+AEKEGLTKLLDPEDVNVDQPD
Sbjct: 241  RDGLAFNAIVHKHRPDLIDFENLKRSNAHYNLQNAFNVAEKEGLTKLLDPEDVNVDQPD 300

Query: 263  EKSIIITYVATYYHYFSKM-MLAVEGKRIGKVLDHAMEAEHLVEKYESLASELLQWIEQTI 321
          EKSIIITYVA YYHYFSKM LAVEGKRIGKVLD+A+EA+ L+EKYE+LASELLQWIEQTI
Sbjct: 301  EKSIIITYVAPYYHYFSKMKALAVEGKRIGKVLDYAIEADQLIEKYETLASELLQWIEQTI 360

Query: 322  GTFNDRQLANSLSGVQNQLQSFNSYRTVEKPPKFTEKGNLEVLLFTIQSKL-MNNQKVYT 380
          T NDRQLANSLS VQNQLQ+FNSYRTVEKPPKFTEKGNLEVLLFTIQSK+ NNQKVY
Sbjct: 361  VTLNDRQLANSLSAVQNQLQAFNSYRTVEKPPKFTEKGNLEVLLFTIQSKMRANNQKVYM 420

Query: 381  PREGRILISDIN-MWERLE-MEHERELALRTELIRQEKLEQL-MRFDR--WMRETWLSNQ 435
          P+EG+LISDIN WERLE EHERELALR ELIRQEKLE L RFDR MRETWLSNQ
Sbjct: 421  PKEGKLISDINKAWERLEKAEHERELALRNELIRQEKLEMLAARFDRKAAMRETWLSNQ 480

Query: 436  RLVSQDNFGLEL--MVEMVRKHEAIETDIVAYSGRVQAVDAVMELMEH--YHDIKRIM-R 490
          RLVSQDNFG L + RKHEAIETDI AY RV AV AV +E YHD++RI+ R
Sbjct: 481  RLVSQDNFGTNLGAEEAATRKHEAIETDIGAYWVERVAAVQAVARELEAEGYHDVRRILAR 540

Query: 491  QNNVARLWDF-XXXXXXXXXXXXXXXXXQKFQDLLYLMDWMAEMKGRQLQSQDLGKHLAG 549
          ++NV RLW++ Q++FQ++ Y+MDWM +MKGRQLQS D GKHL
Sbjct: 541  RDNVLRLEWEYLKELLAARRERLNAHRDLQRLFQEMRYIMDWMGDMKGRQLQSPDSGKHLHD 600

Query: 550  VEDLLQLHELVEADIAVQAERV-MVSASALRFCDPGKEYRPCGPQLVSEVATLEQSYEA 608
          V DLLQ H LVEAD + QAER+ V +A RF + Y+PC P LVSE+V L Q+YE
Sbjct: 601  VLDLLQKHTLVEADSSAQAEIRKAVQGAQRFTSYEQAYKPCPEGLVSEKVDLLGQAYEE 660

Query: 609  LCELMTRMR--LEESRRLWRFLWEVGEAEAWVREQQHLLASAETGRDLTGVLRLLNKHTA 666
          L +L + R LE+SRRLW+FLW+VGE AW+REQ+ +LAS + GRDLT L LL+KH A
Sbjct: 661  LGQLAVKRREQLEDSSRLWQFLWDVGEEAAWIREQEILASGDCGRDLTSALHLLSKHEA 720

Query: 667  LRGEMSGRLGPLKLTLEQGGQLVAEGHPGANQASTXXXXXXXXXXXXXXXXXXXXX-- 724
          R EM+ R GPL ++ G+ L+ EGH GA + +
Sbjct: 721  FRDEMAARYGPLSNSIAVGEALIKEGHFGAPEVRERIEDIRGQWSHLEETSQLEQSLKE 780

Query: 725  --SLYQFQADANDMEAWLVDALRLVSSPEVGHDEFSTQALAR-QHMLEEEIM-HRPTLDA 780
          +L+QFQ DANDMEAW+++ R VSS EVGHDEFSTQ LAR Q +EEEI HRP +D+
Sbjct: 781  SVALHQFQTDANDMEAWIMETFRQVSSQEVGHDEFSTQTLARKQREIEEIKSHRPLIDS 840

Query: 781  LRE--QWLPPALSHTPEVQGRVPTLEQHYEELQAMG----EMMLEMLAFYTMLSEAGACG 834
          L E Q LP A + PEV GR+P +EQ YEEL+++ + + LA Y M SEAGAC
Sbjct: 841  LHEQAQALPQAYVNFPEVDGRLPALIEQRYEELESLSVARRQALEGALALYRMFSEAGACL 900

Query: 835  LWVEEKEQWLNGLALPERLEDPEVVQORFETLEPEMNAL-MRITAVSDIAEQLLSPPG-- 891
          +WVEEKEQ L+G+ +P +LED EVVQORFETLEPEMN L R+T V+ AEQLLS
Sbjct: 901  VWVEEKEQRLHGMEIPTKLEDLEVVQORFETLEPEMNNLGARVTYVNQAEQLLSSDSCN 960

Query: 892  KDRIIGTQEQLNQRWQQFRSLAGGK--GLTSALSIQNYHLECTETQAWMREKTKVIESTQ 949

```

KD+I T++QLN RW++F LAG K L SAL+IQNYHLEC E Q WM+EKTKVISTQ
Sbjct: 961 KDQIHQTRDQLNDRWKEFEQLAGQKKQDLESALNIQNYHLECNEIQTWMEKTKVISTQ 1020

Query: 950 DLGNLAGVLALQRKLAGTERDLEAISARVGELTQEANALM-GHPAQAPAINTRLGEVQT 1008
LGNDLAGV+ALQRKL G ERDLEAI ++ +L EA L HP QA I RL E+Q
Sbjct: 1021 GLGNLAGVMALQRKLTGMERDLEAIQKGKLDLNRNEAEKLAREHPDQAGEIQGRLTEIQE 1080

Query: 1009 GWEDLM-TMRRREESLGEARRLQDFLRSLDDFQAWLGRTQTAVASXXXXXXXXXXXXXXXXX 1067
WEDL TM+RREESLGEA +LQ FLR LDDFQ WL RTQTAVAS
Sbjct: 1081 VWEDLNDTMKRREESLGEASKLQGFLRDLDFFQTWLSRTQTAVASEDIPTSLPEAESLLA 1140

Query: 1068 QH-MLRGEVE-MQSEYSRLRTLGEVTRDQADPQCLFLRQRLEALGTGWEELGRMWESRQ 1125
QH ++ EV+ + +Y ++R +GEEVT+ Q D Q +FL QRL+AL TGW EL RMWE+R
Sbjct: 1141 QHESIKNEVDNYKEDYEKMRAVGEEVTQGQTD AQHMF LAQRLQALDTGWHELRRMWENRH 1200

Query: 1126 GRLAQAHGFQGFRLDARQAEGVLSSQEYVLSHTEMPGTLQ--MDMIKKLEDFMSTMDANG 1183
LAQA FQ FLRDA+QAE L+SQEYVLSHTEMP +LQ + IKK EDF++T +A+
Sbjct: 1201 SLLAQAFDFQTFRLDAKQAEFTLNSQEYVLSHTEMPTSLQGAEEAIKKKHEDFLTTEASE 1260

Query: 1184 ERIRGLLEAGRQLVSKGNIHAEKIQE-MDSIEKRHRKNQEAVQQLGRLRDNREQQHFLQ 1242
E+I ++E+GR+L++ N +++KIQE +DSI +RHRKN+EA +LL +L+DNRE QHFLQ
Sbjct: 1261 EKINSVVESGRRLINDCNANSDKIQEKVDSILERHRKNKEAANELLAKLKNRELQHFLQ 1320

Query: 1243 DCQELKLWIDEKMLTAQDVSYEARNLHTKWQKHQAFMAELM-NKDWLDKVDKEGRELTL 1301
D QEL LWI+EKMLTAQD+SYDEARNLH+KWQKHQAFMAEL NKDWLDK+DKEG+ L
Sbjct: 1321 DGQELTLWINEKMLTAQDMSYEARNLHSHKWQKHQAFMAELASNKDWLDKIDKEGQALVA 1380

Query: 1302 EKPELKVLVSEKLEDLHRRWDELETTTQA-MRSLFDAN-MELFAQSCSALESWLESLOAQ 1359
EKPELK +V + L+DL R+W+ELE TTQ + LFDAN ELF QSCSAL+ WL++L+ Q
Sbjct: 1381 EKPELKPVVEQTLQDLQRQWEELEGGTQTAKAQLFDANRAELFTQSCSALDVWLKNLEGQ 1440

Query: 1360 LHSDDYGKDLTSVNILLKKQOMLEREMAVREKEVEAIQAQALA--QEDQSAGEVE-RTSM 1416
L SDDYGKDLTSVNILLKK QMLE +M VREKEV+++Q+QALA QED EV+ +
Sbjct: 1441 LQSDDYGKDLTSVNILLKKHQMELHQMVEVREKEVQSLQSALALSQEDAGLTEVDGQQR 1500

Query: 1417 VEEKFM-LCQPMKDRCRRLQASREQHQFHRDVEDEILWVTERLPMASLEHGKDLPSVQL 1475
V + F L +P+ R +RL AS+E HQF+RD+EDEILWV ER+P+A+S +HGKDL P+VQL
Sbjct: 1501 VTDNFSNLQEPLNLRRLQRLASKEAHQFNRLDEDEILWVKERMPLATSTDHGKDLPTVQL 1560

Query: 1476 LMKKNQTLQKEIQGHEPRIADLKERQRTLRTWGPE-----LAELQEMWKRLSHELEL 1527
L+KKNQTLQKEIQGH+PRI D+ R +T E L ELQ++W L E +
Sbjct: 1561 LIKKNQTLQKEIQGHQPRIDDIHRRSKTQSQVDGERQSVQEERLCELQDLWSHLIAETDK 1620

Query: 1528 RGKRLEEA-LMQQFYRD-MEAEAWMGEQELHMMGQE--KDELSAQAEVKKHQVLEQALAD 1583
R RL EA QQFY D EAEAWMGEQELHM+ +E KDE SA +KKHQ LEQAL D
Sbjct: 1621 RHTRLIEANRAQQFYADAAEAEAWMGEQELHMLSEEKAKDEQSALVMLKKHQSLEQALE 1680

Query: 1584 YAQTIKQLM-SSQDMIDHEHPESTRLTIRQAQVDKLYAGLKELAGXXXXXXXXXXXXXXXXX 1642
YAQTI QL SS+ M++ E+PES R+T+RQAQVDKLYAGLK+LA
Sbjct: 1681 YAQTIHQLANSSRLMVNSENPESEIRITLQAQVDKLYAGLKDLAEERRGQLQESLRLTQL 1740

Query: 1643 XXXXDDLEQWIQEREVVM-SHELGDYEHVTMLRDKFREFSRDTSTIGQERVDSXXXXXX 1701
DDLEQWI EREV V SHELGDYEHVTMLRDKFRE+RDTSTIGQERVD
Sbjct: 1741 KREVDDLEQWIAEREVVAGSHELGDYEHVTMLRDKFREFAFDTSTIGQERVVDGVNALAD 1800

Query: 1702 XXXXXHMMW-ATVAEWKDSLNEAWADLLELDTRGQVLW--YELQRFHGHARQALARVQH 1758
H+ ++AEWKD LNEAWADLLEL+DTR Q+L YEL RF A + L R++
Sbjct: 1801 DLIESGHIENISIAEWKDGLEAWADLLELDTRTQMLAASYELHRFHQDAMEVLGRIKE 1860

Query: 1759 KQQQLPDGTGRDLN-MEALQRRHCAYEHDIQALSTQVQQVQDDGLRLQ-MYAGD-MEEIG 1815

Sbjct: 1861 KREGLPSDLGRDLNKNVQHLHRQHNTFENDIQALSGQVNQVQDDAARLQKAYAGEKADDIH 1920

Query: 1816 RHMQAVAEAW-AQLOGSSMRRQLLLDITDKFRFF-MVRELMLWMDGINLQMDAQERPRDV 1873
R AV AW L+ RR LL+DT +KFRFF MVR+LMLWMDG+NLQ+DA + PRDV

Sbjct: 1921 RSEHAVISAWEGGLEAGQARRVLLVDITVEKFRFFNMVRDLMLWMDGVNLQIDAHDSPRDV 1980

Query: 1874 SSADLVIKNQGGIM-EIEA-MDRFSACIDMGQELLARNHYM-EEISEKLSQLQSRROETA 1930
SSA LVI N Q I EIE D F+ACI+MG LL NHY +EI EKL QLQ +R++

Sbjct: 1981 SSAGLVIANHQDIKSEIETRADSFACIEMGNTLLNNNHASDEIREKLKQLQEKREKID 2040

Query: 1931 EKWQEKMDWLQVLVLEVLVFGDRDAGM-EAWLCSQEPLVRSaelGCTVDEV-SLIKRHEAFQ 1988
+KWQ+KMD LQ+VLEVL FGRDA + E+WL QEPLVR+AELG VDEV SLIKRHEAF+

Sbjct: 2041 KKWQDKMDHLQIVLEVLQFGRDAYIAESWLAGQEPLVRAELGANVDEVESLIKRHEAFE 2100

Query: 1989 KSAVAWEERFSALEKLTALXXXXXXXXXXXXXXXXXXXXPPTSEPMASQPEGSLVDGQORVL 2048
K A WE+RF LEKLT L P A S +

Sbjct: 2101 KLAAGWEDRFVLLLEKLTLEEQEMQRRREEERARRPPTPPPAEEAVDMTESHIHDS--- 2157

Query: 2049 DTAWDGTQSKL-PPS-----TQAPSINGVCTDTESSQ-----PLLEQQRLEQSN 2091
A Q++L PPS + P I + S L + + +S

Sbjct: 2158 -AARPCEQARLFPPSKFHDFSHLPVIGCSSARSHPSYRVFSRSPPTLFLRPQGESE 2216

Query: 2092 XPEGPGSGTGDESSGPRGERQTLPRGPAPSPMPQSRSSSAHVATLPARGAELSAQEOME 2151
GPG +G SS R A + P +ES E ME

Sbjct: 2217 SVNGPGRDGLASS-----RLEASATLPNRGGAES-----EPEAME 2252

Query: 2152 GTLCRKQEMEAFNK---NRSWQNVYCVLRGSLGFYKDAWSA--GVPHYGEVPVSLAMQ- 2205
G LCRKQEME+ +K RSWQNVYCVLR+GSLGFYKD SA G+PHYGEVP+SLA

Sbjct: 2253 GMLCRKQEMESHKKAATRSWQNVYCVLRKGSGLGFYKDGKSASNGIPYHGEVPISLAEAV 2312

Query: 2206 GSVAFDYRKRKHVFKLGLQDGKEYLFQAKDEAEMSSWLRVNMIATASSASGE-PEEPVV 2264
VA DY+KRKHVFKL L DGKEYLFQAKDEAEM SW+R +++ + S SG+ P P V

Sbjct: 2313 CEVAHDYKKRKHVFKLRLRGDGKEYLFQAKDEAEMGSWIR--SILGSVPSGSGDSPGGPRV 2370

Query: 2265 PSASRGLTMMTPPVSQPEGSIIVLRSKDG 2293
SR +TM + P S G + +R+KDG

Sbjct: 2371 --LSRAMTMPPISPSSAEGGVMTMRNKDG 2397

 >gi|38084794|ref|XP_129130.3|  spectrin beta 3 [Mus musculus]
Length = 2409

Score = 3411 bits (8844), Expect = 0.0

Identities = 2074/2393 (86%), Positives = 2090/2393 (87%), Gaps = 100/2393 (4%)

Query: 1 MSSTLSPTDFDSLEIQGQYSDINNRRWDLPSDWDNDSSSARLFERSRI----- 48
MSSTLSPTDFDSLEIQGQYSDINNRRWDLPSDWDNDSSSARLFERSRI

Sbjct: 1 MSSTLSPTDFDSLEIQGQYSDINNRRWDLPSDWDNDSSSARLFERSRIKALAAAFINPAQ 60

Query: 49 -----MLADEREAVQKKTFTKWVNSHLARVTCRVGDLYSXXXXXXXXXXXXXEVLS 98
L DEREAVQKKTFTKWVNSHLARVTCRVGDLYS EVLS

Sbjct: 61 YASVLEGRFKQLQDEREAVQKKTFTKWVNSHLARVTCRVGDLYSDLRDGRNLLRLLEVLS 120

Query: 99 GETLPKPTKGRMRIHCLENVD--LQFLKEQKVHLENMGSHDIVDGNHRLTLGLVWTIILR 156
GETLPKPTKGRMRIHCLENVD LQFLKEQKVHLENMGSHDIVDGNHRLTLGLVWTIILR

Sbjct: 121 GETLPKPTKGRMRIHCLENVDKALQFLKEQKVHLENMGSHDIVDGNHRLTLGLVWTIILR 180

Query: 157 FQIQDISVETEDNKEKKSADALLWCQMKTAGYPNVNVHNFTTSWRDGLAFNAIVHKHR 216

Sbjct: 181 FQIQDISVETEDNKEKKSAKDALLLWCQMKTAGYPNVNVHNFTTSWRDGLAFNAIVHKHR 240

Query: 217 PDLLDFESLKKCNAYNLQNAFNLAKEKLGTLKLLDPEDVNVDPDEKSIITYVATYYHY 276
PDLLDFESLKKCNAYNLQNAFNLAKEKLGTLKLLDPEDVNVDPDEKSIITYVATYYHY

Sbjct: 241 PDLLDFESLKKCNAYNLQNAFNLAKEKLGTLKLLDPEDVNVDPDEKSIITYVATYYHY 300

Query: 277 FSKM-MLAVEGKRIGKVLHDHAMEAEHLVEKEYESLASELLQWIEQTIGTFNDRQLANSLSG 335
FSKM LAVEGKRIGKVLHDHAMEAEHLVEKEYESLASELLQWIEQTI T NDRQLANSLSG

Sbjct: 301 FSKMKALAVEGKRIGKVLHDHAMEAEHLVEKEYESLASELLQWIEQTIVTLNDRQLANSLSG 360

Query: 336 VQNQLQSFNSYRTVEKPPKFTEKGNLEVLLFTIQSKL-MNNQKVYTPREGRLISDIN-MW 393
VQNQLQSFNSYRTVEKPPKFTEKGNLEVLLFTIQSKL NNQKVYTPREGRLISDIN W

Sbjct: 361 VQNQLQSFNSYRTVEKPPKFTEKGNLEVLLFTIQSKLRANNQKVYTPREGRLISDINKAW 420

Query: 394 ERLE-MEHERELALRTELIRQEKLEQL-MRFDR--WMRETWLSNQRLVSQDNFGLELMV 449
ERLE EHERELALRTELIRQEKLEQL RFDR MRETWLSNQRLVSQDNFGLEL

Sbjct: 421 ERLEKAEHERELALRTELIRQEKLEQLAARFDRKAAMRETWLSNQRLVSQDNFGLELAA 480

Query: 450 --EMVRKHEAIETDIVAYSGRVQAVDAVMELM--EHYHDIKRI-MRQNNVARLWDF-XXX 503
VRKHEAIETDIVAYSGRVQAVDAV + EHYHDIKRI RQNNVARLWDF

Sbjct: 481 VEAARVRKHEAIETDIVAYSGRVQAVDAVAELAAEHYHDIKRIAARQNNVARLWDFLRQM 540

Query: 504 XXXXXXXXXXXXXXXQKVFQDLLYLMDWMAEMKGRQLQSQDLGKHLAGVEDLLQLHELVEAD 563
QKVFQDLLYLMDWMAEMKGRQLQSQDLGKHLAGVEDLLQLHELVEAD

Sbjct: 541 VAARRERLLLNLLELQKVFQDLLYLMDWMAEMKGRQLQSQDLGKHLAGVEDLLQLHELVEAD 600

Query: 564 IAVQAERV-MVSASALRFCDPGKEYRPCGPQLVSERVATLEQSYEALCELMT--RMRLEE 620
IAVQAERV VSASALRFCDPGKEYRPC PQLVSERVATLEQSYEALCEL R LEE

Sbjct: 601 IAVQAERVRAVSASALRFCDPGKEYRPCDPQLVSERVATLEQSYEALCELAATRRARLEE 660

Query: 621 SRRLWRFLWEVGEAEAWVREQQHLLASAETGRDLTGVLRLLNKHTALRGEMSGRLGPLKL 680
SRRLWRFLWEVGEAEAWVREQQHLLASA+TGRDLTGVLRLLNKH ALRGEMSGRLGPLKL

Sbjct: 661 SRRLWRFLWEVGEAEAWVREQQHLLASADTGRDLTGVLRLLNKHAALRGEMSGRLGPLKL 720

Query: 681 TLEQGQQLVAEGHPGANQASTXXXXXXXXXXXXXXXXXXXXM---SLYQFQADANDM 736
TLEQGQQLVAEGHPGANQAST + SLYQFQADANDM

Sbjct: 721 TLEQGQQLVAEGHPGANQASTRAELQAQWERLEALAEERAQQLAQAAASLYQFQADANDM 780

Query: 737 EAWLVDALRLVSSPEVGHDEFSTQALARQH-MLEEEI-MHRPTLDALREQ--WLPPALSH 792
EAWLVDALRLVSSPEVGHDEFSTQALARQH LEEI HRPTLDALREQ LPPALSH

Sbjct: 781 EAWLVDALRLVSSPEVGHDEFSTQALARQHRALEEEI RAHRPTLDALREQAAALPPALSH 840

Query: 793 TPEVQGRVPTLEQHYEELQAMG----EMMLELAFYTMSEAGACGLWVEEKEQWLNGLA 848
TPEVQGRVPTLEQHYEELQA + LAFYTMSEAGACGLWVEEKEQWLNGLA

Sbjct: 841 TPEVQGRVPTLEQHYEELQARAGERARALEAALAFYTMSEAGACGLWVEEKEQWLNGLA 900

Query: 849 LPERLEDPEVVQORFETLEPEMNAL-MRITAVSDIAEQLL--SPPGKDRIIGTQEQLNQR 905
LPERLED EVVQORFETLEPEMNAL R+TAV+DIAEQLL SPPGKDRIIGTQEQLNQR

Sbjct: 901 LPERLEDLEVVQORFETLEPEMNALAARVTAVNDIAEQLLKASPPGKDRIIGTQEQLNQR 960

Query: 906 WQQFRSLAGGK--GLTSALSIQNYHLECTETQAWMREKTKVIESTQDLGNDLAGVLALQR 963
WQQFRSLA GK LTSALSIQNYHLECTETQAWMREKTKVIESTQ LGNDLAGVLALQR

Sbjct: 961 WQQFRSLADGKKAALTSALSIQNYHLECTETQAWMREKTKVIESTQGLGNDLAGVLALQR 1020

Query: 964 KLAGTERDLEAISARVGELTQEANAL-MGHPAQAPAINTRLGEVQTGWEDL-MTMRREE 1021
KLAGTERDLEAISARVGELTQEANAL GHPAQAPAINTRLGEVQ GWEDL TMRREE

Sbjct: 1021 KLAGTERDLEAISARVGELTQEANALAAGHPAQAPAINTRLGEVQAGWEDLRATMRREE 1080

Query: 1022 SLGEARRLQDFLRSLDDFQAWLGRTQTAVASXXXXXXXXXXXXXQH-MLRGEVE-MQS 1079

Sbjct: 1081 SLGEARRLQDFLRSLLDDFQAWLGRTQTAVAS QH LRGEVE QS 1140

Query: 1080 EYSRLRTLGEDEVTRDQADPQCLFLRQRLEALGTGWHEELGRMWESRQGRLAQAHGFQGFLLR 1139
EYSRLRTLGEDEVTRDQADPQCLFLRQRLEALGTGWHEELGRMWESRQGRLAQAHGFQGFLLR

Sbjct: 1141 EYSRLRTLGEDEVTRDQADPQCLFLRQRLEALGTGWHEELGRMWESRQGRLAQAHGFQGFLLR 1200

Query: 1140 DARQAEGVLSSQYVLSHTEMPGTLQ--DMIKKLEDFMSTMDANGERIRGLLEAGRQLV 1197
DARQAEGVLSSQYVLSHTEMPGTLQ IKKLEDFMSTMDANGERIRGLLEAGRQLV

Sbjct: 1201 DARQAEGVLSSQYVLSHTEMPGTLQAADAAIKKLEDFMSTMDANGERIRGLLEAGRQLV 1260

Query: 1198 SKGNIHAEKIQE-MDSIEKRHRKNQEAQVQLLGRRLDNREQQHFLQDCQELKLWIDEKML 1256
SKGNIHAEKIQE DSIKRHRKNQEAQVQLLGRRLDNREQQHFLQDCQEL+LWIDEKML

Sbjct: 1261 SKGNIHAEKIQEKADSIKRHRKNQEAQVQLLGRRLDNREQQHFLQDCQELRLWIDEKML 1320

Query: 1257 TAQDVSIDEARNLHTKWQKHQAFMAEL-MNKDWLDKVDKEGRELTLEKPELKVIVSEKLE 1315
TAQDVSIDEARNLHTKWQKHQAFMAEL NKDWLDKVDKEGRELTLEKPELKV+VSEKLE

Sbjct: 1321 TAQDVSIDEARNLHTKWQKHQAFMAELAANKDWLDKVDKEGRELTLEKPELKVVVSEKLE 1380

Query: 1316 DLHRRWDELETTTQA-MRSLFDAN-MELFAQSCSALESWLESQAQLHSDDYGKDLTSVN 1373
DLHRRWDELETTTQA RSLFDAN ELFAQSCSALESWLESQAQLHSDDYGKDLTSVN

Sbjct: 1381 DLHRRWDELETTTQAKARSFLDANRAELFAQSCSALESWLESQAQLHSDDYGKDLTSVN 1440

Query: 1374 ILLKKQQMLEREMAVREKEVE--AIQAQALAQEDQSAGEVERTS-MVEEF-MLCQPMKD 1429
ILLKKQQMLEREMAVREKEVE QAQALAQEDQSAGEVERTS VEEKF LCQPMK+

Sbjct: 1441 ILLKKQQMLEREMAVREKEVEAIQAQALAQEDQSAGEVERTSRAVEEFKRALCQPMKE 1500

Query: 1430 RCRRLQASREQHQFHRDVEDEILWVTERLPMASLEHGKDLPSVQLLMKKNQTLQKEIQG 1489
RCRRL ASREQHQFHRDVEDEILWVTERLPMASLEHGKDLPSVQLLMKKNQTLQKEIQG

Sbjct: 1501 RCRRLHASREQHQFHRDVEDEILWVTERLPMASLEHGKDLPSVQLLMKKNQTLQKEIQG 1560

Query: 1490 HEPRIADLKERQRTLRT--WGPELAELQEMWKRLSHELELRGKRLEEAL-MQQFYRD-ME 1545
HEPRIADLKERQRTL T GPELAELQEMWKRLSHELELRGKRLEEAL QQFYRD E

Sbjct: 1561 HEPRIADLKERQRTLGTAAAGPELAELQEMWKRLSHELELRGKRLEEALRAQQFYRDAE 1620

Query: 1546 AEAWMGEQELHMMGQE--KDELSAQAEVKKHQVLEQALADYAQTIKQL-MSSQDMIDHEH 1602
AEAWMGEQELHMMGQE KDELSAQAEVKKHQVLEQALADYAQTIKQL SSQDMIDHEH

Sbjct: 1621 AEAWMGEQELHMMGQEKAKDELSAQAEVKKHQVLEQALADYAQTIKQLAASSQDMIDHEH 1680

Query: 1603 PESTRLTIRQAQVDKLYAGLKELAGXXXXXXXXXXXXXXXXXXXXDDLEQWIQEREVV-MS 1661
PESTRLTIRQAQVDKLYA LKELAG DDLEQWIQEREVV S

Sbjct: 1681 PESTRLTIRQAQVDKLYASLKELAGERRERLQEHLRLCQLRRELDLEQWIQEREVVAAS 1740

Query: 1662 HELGQDYEHVTMLRDKFREFSRDTSTIGQERVDSXXXXXXXXXXXXXHMW-ATVAEWKDSL 1720
HELGQDYEHVTMLRDKFREFS+DTSTIGQERVDS H ATVAEWKDSL

Sbjct: 1741 HELGQDYEHVTMLRDKFREFSKDTSTIGQERVDSANALANGLIAGGHAARATVAEWKDSL 1800

Query: 1721 NEAWADLLELLDTRGQVL--WYELQRFHGARQALARVQHKQQQLPDGTGRDLN-MEALQ 1777
NEAWADLLELLDTRGQVL YELQRFHGARQALARVQHKQQQLPDGTGRDLN EALQ

Sbjct: 1801 NEAWADLLELLDTRGQVLAAAYELQRFHGARQALARVQHKQQQLPDGTGRDLNAAEALQ 1860

Query: 1778 RRHCAYEHDIQALSTQVQQVQDDGLRLQ-MYAGD-MEEIGRHMQAVAEAWAQLQGSS-MR 1834
RRHCAYEHDIQALSTQVQQVQDDG RLQ YAGD EEIGRHMQAVAEAWAQLQGSS R

Sbjct: 1861 RRHCAYEHDIQALSTQVQQVQDDGQRLQKAYAGDKAEIIGRHMQAVAEAWAQLQGSSAAR 1920

Query: 1835 RQLLLDTTDKFRFF-MVRELMLWMDGINLQMDAQERPRDVSSADLVKNQQGI-MEIEA- 1891
RQLLLDTTDKFRFF VRELMLWMDGINLQMDAQERPRDVSSADLVKNQQGI EIEA

Sbjct: 1921 RQLLLDTTDKFRFFKAVRELMLWMDGINLQMDAQERPRDVSSADLVKNQQGIKAEIEAR 1980

Query: 1892 MDRFSACIDMGQELLARNHY-MEEISEKLSQLQSRQETAEKWQEKMDWLQVLVLEVLVFG 1950

DRFS+CIDMGQELLAR+HY EEISEKLSQLQSRQETA+KWQEKMDWLQLVLEVLVFG
 Sbjct: 1981 ADRFSSCIDMGQELLARSHYAAEEISEKLSQLQSRQETADKWQEKMDWLQLVLEVLVFG 2040

Query: 1951 RDAGM-EAWLCSQEPLVRSaelGCTVDEV-SLIKRHEAFQKSAVAWEERFSALEKLTALX 2008
 RDAGM EAWLCSQEPLVRSaelGCTVDEV SLIKRHEAFQKSAVAWEERFSALEKLTAL
 Sbjct: 2041 RDAGMAEAWLCSQEPLVRSaelGCTVDEVESLIKRHEAFQKSAVAWEERFSALEKLTAL 2100

Query: 2009 XXXXXXXXXXXXXXXXXXXXPPTSEPMASQPEGSLVDGQRVLDTAWDGTQSKLPPSTQAPSI 2068
 PPTSEPMASQPEGSLVDGQRV DTAWDGTQSKLPPSTQAPS+
 Sbjct: 2101 ERENERKRKREEEERRKQPPTSEPMASQPEGSLVDGQRVDPDTAWDGTQSKLPPSTQAPSV 2160

Query: 2069 NGVCTDTESSQPLLEQQRLQSNXPEGPGSGTGDESSGPRGERQTLPRGPAPSPMPQSRS 2128
 NGVCTDT+SSQPLLEQQRLQSN PEGPGSGTGDESSGPRGERQTLPRGPAPSPMPQSRS
 Sbjct: 2161 NGVCTDTESSQPLLEQQRLQSNVPEGPGSGTGDESSGPRGERQTLPRGPAPSPMPQSRS 2220

Query: 2129 SESAHVATLPARGAELSAQEQQMEGTLCKRKQEMEAFNK---NRSWQNVYCVLRRGSLGFYK 2185
 SE+AH ATLP RG ELSAQEQMEG LCKRKQEMEAFNK NRSWQNVYCVLRRGSLGFYK
 Sbjct: 2221 SEAAHGATLPTRGPELSAQEQMEGMLCKRKQEMEAFNKKAANRSWQNVYCVLRRGSLGFYK 2280

Query: 2186 D--AWSAGVPYHGEVPVSLA-MQGSVAFDYRKRVFKLGLQDGKEYLFQAKDEAEMSSW 2242
 D A SAGVPYHGEVPVSLA QGSVAFDYRKRVFKLGLQDGKEYLFQAKDEAEMSSW
 Sbjct: 2281 DARAASAGVPYHGEVPVSLARAQGSVAFDYRKRVFKLGLQDGKEYLFQAKDEAEMSSW 2340

Query: 2243 LRVVN-MIATASSASGEPEEPVPSASRGLT-MMTMPPVSQPEGSIVLRSKDG 2293
 LRVVN IATASSA GE EEPVPSASRGLT MTMPPVSQPEGSIVLRSKDG
 Sbjct: 2341 LRVVNAIATASSAPGESEEPVPSASRGLTRAMTMTMPPVSQPEGSIVLRSKDG 2393

☐ >gi|31201699|ref|XP_309797.1| ENSANGP00000023406 [Anopheles gambiae]
 gi|30178366|gb|EAA45309.1| ENSANGP00000023406 [Anopheles gambiae str. PEST]
 Length = 2362

Score = 1576 bits (4081), Expect = 0.0

Identities = 1052/2351 (44%), Positives = 1437/2351 (61%), Gaps = 117/2351 (4%)

Query: 25 RWD-----LPDSDWDNDSSSARLFERSRI-MLADEREAVQKKTFTKWVNSHLARVT 74
 RWD + D ++D +SS+RLFERSRI LA+ERE+VQKKTFTKWVNSHL RV
 Sbjct: 9 RWDPSQGPNGEFIEDIEYDGGNSSSRLFERSRIKALAEERESVQKKTFTKWVNSHLVRVN 68

Query: 75 CRVGDLYSXXXXXXXXXXXXEVLSETLPKPTKGRMRIHCLENVD--LQFLKEQKVHLEN 132
 + DLY EVLSGE LP+PTKG+MRIHCLENVD LQFL+EQ+VHLEN
 Sbjct: 69 SPIKDLYVDMRDGKNLIKLEVLSEGERLPRPTKGKMRIHCLENVDKALQFLREQRVHLEN 128

Query: 133 MGSHDIVDGNHRLTLGLVWTIILRFQIQDISVETEDNKEKKSADALLWCQMKTAGYPN 192
 +GSHDIVDGN L LGL+WTIILRFQIQDI++E DNKE KSAKDALLWCQMKTAGY N
 Sbjct: 129 IGSHDIVDGNASNLGLIWTIILRFQIQDITIEETDNKETKSAKDALLWCQMKTAGYHN 188

Query: 193 VNVHNFTTSWRDGLAFNAIVHKHRPDLIDFESLKKCNAYNLQNAFNLAEKELGLTKLLD 252
 VNV NFTTSWRDGLAFNAI+HKHRPDL+ F+ L K N NL NAFN+AE++LGLTKLLD
 Sbjct: 189 VNVNFTTSWRDGLAFNAIHKHRPDLIQFDKLSKTNPIQNLNNAFNVAEEKLGLTKLLD 248

Query: 253 PEDVNVDQPDEKSIITYVATYYHYFSKM-MLAVEGKRIGKVLDHAMEAEHLVEKYESLAS 311
 ED+ VD PDEKSIITYV TYYHYFSK+ V+GKRIGKV+ AM+ + ++ +YESL S
 Sbjct: 249 AEDIFVDHPDEKSIITYVVVYYHYFSKLQETVQGKRIGKVVGIAMDNDRMINEYESLTS 308

Query: 312 ELLQWIEQTIGTFNDRQLANSLSGVQNQLQSFNSYRTVEKPPKFTEKGNLEVLLFTIQSK 371
 ELL+WIE TI DR NSL GVQ QL F++YRTVEKPPKF EKGNEVLLFT+QSK
 Sbjct: 309 ELLKWIEVTIVQLGDRHFVNSLVGVQQQLAQFSNYRTVEKPPKFVEKGNLEVLLFTLQSK 368